OIPE



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/888,370

DATE: 12/04/2001 TIME: 08:52:35

Input Set : N:\Crf3\RULE60\09888370.raw Output Set: N:\CRF3\12042001\I888370.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:

ENTERED

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5
             (i) APPLICANT: Glimcher, Laurie H. et al.
      7
            (ii) TITLE OF INVENTION: Human c-Maf Compositions and
                                      Methods of Use Thereof
      8
     10
           (iii) NUMBER OF SEQUENCES: 2
            (iv) CORRESPONDENCE ADDRESS:
     12
                   (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
     13
                   (B) STREET: 28 State Street
     14
     15
                  (C) CITY: Boston
                   (D) STATE: Massachusetts
     16
     17
                   (E) COUNTRY: USA
                  (F) ZIP: 02109
     18
             (V) COMPUTER READABLE FORM:
     20
     21
                   (A) MEDIUM TYPE: Floppy disk
     22
                   (B) COMPUTER: IBM PC compatible
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     23
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
     24
     26
            (vi) CURRENT APPLICATION DATA:
                   (A) APPLICATION NUMBER: US/09/888,370
C--> 27
C--> 28
                   (B) FILING DATE: 22-Jun-2001
     29
                   (C) CLASSIFICATION:
     31
           (vii) PRIOR APPLICATION DATA:
                   (A) APPLICATION NUMBER: US/09/086,010
     32
     33
                   (B) FILING DATE:
     34
                   (A) APPLICATION NUMBER: 09/030,579
     35
                  (B) FILING DATE: 2-FEB-1998
     37
          (viii) ATTORNEY/AGENT INFORMATION:
     38
                   (A) NAME: Kara, Catherine J.
                  (B) REGISTRATION NUMBER: 41,106
     39
                   (C) REFERENCE/DOCKET NUMBER: HUI-027CP
     40
            (ix) TELECOMMUNICATION INFORMATION:
     42
     43
                  (A) TELEPHONE: (617)227-7400
                  (B) TELEFAX: (617)742-4214
     44
        (2) INFORMATION FOR SEQ ID NO: 1:
     47
     49
             (i) SEQUENCE CHARACTERISTICS:
     50
                   (A) LENGTH: 1203 base pairs
     51
                  (B) TYPE: nucleic acid
     52
                  (C) STRANDEDNESS: single
     53
                  (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: cDNA
     55
     58
            (ix) FEATURE:
                  (A) NAME/KEY: CDS
     59
     60
                   (B) LOCATION: 1..1203
     63
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     65 ATG GCA TCA GAA CTG GCA ATG AGC AAC TCC GAC CTG CCC ACC AGT CCC
                                                                                   48
     66 Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
```



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Input Set : N:\Crf3\RULE60\09888370.raw
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67	1				5					10					15		
	CTG	GCC	ATG	GAA	_	GTT	AAT	GAC	TTC		CTG	ATG	AAG	TTT		GTG	96
	Leu																
71				20	- 4 -				25				•	30			
73	AAA	AAG	GAA	CCG ·	GTG	GAG	ACC	GAC	CGC	ATC	ATC	AGC	CAG	TGC	GGC	CGT	144
74	Lys	Lys	Glu	Pro	Val	Glu	Thr	Asp	Arg	Ile	Ile	Ser	Gln	Cys	Gly	Arg	
75	-	_	35					40	_				45				
77	CTC	ATC	GCC	GGG	GGC	TCG	CTG	TCC	TCC	ACC	CCC	ATG	AGC	ACG	CCC	TGC	192
78	Leu	Ile	Ala	Gly	Gly	Ser	Leu	Ser	Ser	Thr	Pro	Met	Ser	Thr	Pro	Cys	
79		50					55					60					
	AGC																240
82	Ser	Ser	Val	Pro	Pro		Pro	Ser	Phe	Ser	Ala	Pro	Ser	Pro	Gly		
83	65					70					75					80	
	CGA																288
	Arg	Gly	Glu	Gln		Ala	His	Leu	Glu		Tyr	Tyr	Trp	Met		Gly	
87					85					90		:			95		226
	TAC																336
	Tyr	Pro	GIn		Leu	Asn	Pro	GLu		Leu	GTĀ	Pne	ser		GIU	Asp	
.91				100	-		. a á		105	a. a		·		110	000	mma	204
	GCG																384
	Ala	vaı		Ala	Leu	шe	ser		ser	HIS	GIII		125	СТУ	GIY	Phe	
95	GAT	ccc	115	CCC	CCC	ccc	CCC	120	CAC	сπл	CCC			CCC	GGG	GCA	432
	Asp																452
99	ASP	130	тут	Ата	ALY	СТУ	135	GIII	GIII	пеа	AIG	140	лти	AIG	GLY	AIG	
	1 (601		- GGC	י פכר	י ייירכר	י יייים		GGC	AGC	GGC	' GAG	-	ΑΤО	GGC	c ddd	GCC	480
																Ala	
	3 145		. 0-1			150	_	- 1		1	155			2		160	
			GTG	GTG	TCC			ATC	: GCC	GCG	GCC	GCC	GCC	CAC	AGC	GGC	528
																Gly	
10					165					170					175		
109	GCG	GGG	CCG	CAC	TAC	CAC	CAC	CAC	CAC	CAC	CAC	GCC	GCC	GGC	CAC	CAC	576
110) Ala	Gly	Pro	His	Tyr	His	His	His	His	His	His	Ala	Ala	Gly	/ His	His	
11:				180					185					190			
																CGCT	624
114	4 His	s His	s Pro	Thr	Ala	. Gly	Ala	Pro	Gly	Ala	Ala	Gly			a Ala	ı Ala	
11			195					200					205				
																GTT	672
			_	Gly	Ala	Gly			Gly	Gly	Gly) Ala	a Ser	. Val	
119		210		_			215					220					700
																GCG	720
			z Glv	7 (2) 3	CIV	. GTÀ	GIY	GTA	GIY	GI			GT2	Y GIZ	Ala	Ala 240	
			O T J	O ₁	0-1												
	3 225	5				230					235		030	n mme	י כאכ		760
12	3 225 5 GGC	G GCC	CTG	CAC	CCG	230 CAC	CAC				GGC	CTG				GAC	768
12: 12:	3 225 5 GGC 6 Gly	G GCC	CTG	CAC	CCG	230 CAC His	CAC			Gly	GGC Gly	CTG			e Asp	GAC Asp	768
12: 12: 12:	3 225 5 GGC 6 Gly 7	G GCC 7 Ala	C CTG	CAC His	CCG Pro	230 CAC His	CAC His	Ala	Ala	Gly 250	GGC Gly	CTG Leu	His	s Phe	255	GAC Asp	
12: 12: 12: 12:	3 225 5 GGC 6 Gl _y 7 9 CGC	G GCC Ala	C CTG	CAC His	CCG Pro 245	230 CAC His	CAC His CTG	Ala	Ala	Gly 250	GGC Gly	CTG Leu GTG	His	S Phe	Asp 255 TGG	GAC Asp AAC	768
12: 12: 12: 12:	3 225 5 GGC 6 Gl _y 7 9 CGC 0 Arg	G GCC Ala	C CTG	CAC His	CCG Pro 245 GAG	230 CAC His	CAC His CTG	Ala	Ala	Gly 250 ATO Met	GGC Gly	CTG Leu GTG	His	S Phe	255 255 TGG Trp	GAC Asp	



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133	CGG	CAG	CTG	CGC	GGG	GTC	AGC	AAG	GAG	GAG	GTG	ATC	CGG	CTG	AAG	CAG	864
134	Arg	Gln	Leu	Arg	Gly	Val	Ser	Lys	Glu	Glu	Val	Ile	Arg	Leu	Lys	Gln	
135			275					280					285				
			CGG														912
138	Lys	Arg	Arg	Thr	Leu	Lys	Asn	Arg	Gly	\mathtt{Tyr}	Ala	Lys	Ser	Cys	Arg	Phe	
139		290					295					300					
			GTG														960
142	Lys	Arg	Val	Gln	Gln	Arg	His	Val	Leu	Glu	Ser	Glu	Lys	Asn	Gln	Leu	
143	305					310					315					320	
			CAA														1008
146	Leu	Gln	Gln	Val	Asp	His	Leu	Lys	Gln	Glu	Ile	Ser	Arg	Leu	Val	Arg	
147					325					330					335		
			GAC														1056
150	Glu	Arg	Asp	Ala	Tyr	Lys	Glu	Lys	\mathtt{Tyr}	Glu	Lys	Leu	Val	Ser	Ser	Gly	
151				340			•		345					350			
			GAA														1104
	Phe	Arg	Glu	Asn	Gly	Ser	Ser	Ser	Asp	Asn	Pro	Ser		Pro	Glu	Phe	
155			355					360					365				•
			ACT														1152
	Phe		Thr	Glu	Pro	Thr	_	Lys	Leu	Glu	Pro		Val	Gly	\mathtt{Tyr}	Ala	
159		370					375					380	•				
			TGG														1200
		Phe	\mathtt{Trp}	Lys	Pro		His	Arg	Val	Leu		Ser	Val	Phe	Thr		
163						390					395					400	
	TGA																1203
	(2)		ORMA														
172		(i)) SEC	_													
173			•	•				nino	acı	ıs							
174			•	•			no ac									•	
175			•	•			line										
177) MOI				_		100	- N	. o						
179	14-4		SE										Dmo	mh m	Com	Dwo	
		Ата	Ser	GIU	ьеu 5	Ата	Met	Ser	ASII	10	Asp	ьeu	PIO	THE	15	PIO	
182	1	210	Wot	C1.,	_	Wa 1) an	λαη	Dho		T 011	Wo+	T ***	Dho		Wa 1	
185	ьец	Ата	Met	20	тут	Val	ASII	АБР	25	АЗР	пеп	Met	пуз	30	GIU	Val	
	Lare	Tve	Glu	-	Val	Glu	Thr	λen		T1_	T10	Sar	Gln		Glv	Δra	
188	пуз	пуз	35	FIO	Val	GIU	T 11T	40	пта	110	110	261	45	Cys	GIY	Arg	
	T.An	Tla	Ala	Glv	Glv	Sar	Τ.Δ11		Sar	ጥከተ	Dro	Mat		Thr	Dro	Cve	
191	Deu	50	пта	GIY	GLY	Der	55	Der	261	T 11T	110	60	Der	1111	FIQ	Cys	
	Ser		Val	Pro	Pro	Ser		Ser	Phe	Ser	Δla		Ser	Pro	Glv	Ser	
	65	001	• • • •			70		001		001	75		501		01	80	
		Glv	Glu	Gln	Lvs		His	Leu	G1u	Asp		Tvr	Trp	Met.	Thr		
197	9	1		~	85					90	-1-	-1-			95	J-1	
	Tvr	Pro	G] n	G] n		Asn	Pro	G] 11	Ala		G] v	Phe	Ser	Pro		Asp.	
200				100					105		1			110		F ,	
		Val	Glu		Leu	Ile	Ser	Asn		His	Gln	Leu	Ara		Glv	Phe	
203			115					120					125	- 4	-1	_	
	Asp	Glv		Ala	Ara	Glv	Ala		Gln	Leu	Ala	Ala	Ala	Ala	Glv	Ala	
203		- 1	- , -			1									1		





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206		130					135					140				
208	Gly	Ala	Gly	Ala	Ser	Leu	Gly	Gly	Ser	Gly	Glu	Glu	Met	Gly	Pro	Ala
	145					150					155					160
	Ala	Ala	Val	Val		Ala	Val	Ile	Ala		Ala	Ala	Ala	Gln		Gly
212					165					170		_	_		175	
	Ala	Gly	Pro		Tyr	His	His	His		His	His	Ala	Ala		His	His
215		1	_	180		a 1	- 1 -		185	- 1 -		a 1	a	190	. 1 -	
	His	His		Thr	Ala	GLY	Ala	Pro	GLY	Ala	Ala	GLY		Ата	Ата	Ата
218	a	. 1 -	195	a 1		a 1	a 1	200	a1	a1	a1	01	205	31-	g	37m 1
	ser		GIY	GIY	Ата	GIY	215	Ala	GIY	GIY	СТУ	220	Pro	Ala	ser	vaı
221	C1	210	C1	C1**	C1**	C1**		Gly	C111	C117	C1 17		Glw	Clv	λla	λla
	225	GLY	GIY	GLY	GLY	230	GLY	СТУ	GIY	СТУ	235	СТУ	GIY	GIY	AIG	240
		Δla	T.en	His	Pro		His	Ala	Δla	Glv		Leu	His	Phe	Asp	
227	011		LCu		245					250	011				255	
	Arq	Phe	Ser	Asp	Glu	Gln	Leu	Val	Thr	Met	Ser	Val	Arg	Asp	Trp	Asn
230	_			260					265				_	270	_	
232	Arg	Gln	Leu	Arg	Gly	Val	Ser	Lys	Glu	Glu	Val	Ile	Arg	Leu	Lys	Gln
233			275					280					285			
235	Lys	Arg	Arg	Thr	Ļeu	Lys	Asn	Arg	Gly	\mathtt{Tyr}	Ala	_	Ser	Cys	Arg	Phe
236		290					295					300				
	-	Arg	Val	Gln	Gln		His	Val	Leu	Glu		Glu	Lys	Asn	Gln	
	305	_				310	_				315	_	_	_		320
	Leu	Gln	Gln	Val	_	His	Leu	Lys	Gln		Ile	Ser	Arg	Leu		Arg
242	a 1	_			325	.	a 1	.		330	T	T	*** 1	0	335	a 1
	GIU	Arg	Asp		Tyr	гĀЗ	GIU	Lys	345	GIU	гÃг	Leu	vaı	350	ser	GIY
245	Dh.	7	a 1	340	C1	C	000	000		7	Dwo	Com	Com		C1	Dho
247	Pile	AIG	355	ASII	СТА	ser	Set	Ser 360	ASP	ASII	PIO	ser	365	PIO	GIU	FIIE
	Dho	т1Д		Glu	Dro	Thr	Δra	Lys	T.A11	Glu	Pro	Ser		Glv	Τυγ	Δla
251	FIIC	370	1111	JIU	-10	1111	375	כעם	<u> </u>	JIU		380	,41		-1-	
	Thr		Trp	Lvs	Pro	Gln		Arg	Val	Leu	Thr		Val	Phe	Thr	Lvs
	385			-, -		390		9			395		· -			400





VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09888370.raw Output Set: N:\CRF3\12042001\1888370.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]